AMENDMENTS TO THE SPECIFICATION

In the Specification

At page 12, lines 17-33, please replace the paragraph with the following:

Expression of the nucleic acid sequence according to the present invention may be achieved by combination of the sequence with a suited promoter. The promoter available in this combination may be the TT1 promoter according to SEQ ID NO:1 as well as a different endogenous promoter of the transformed cell or exogenous promoter from the vector. A suitable promoter is thereby in principle any regulatory sequence, which may regulate the expression of foreign genes in cells, particularly in plants, e.g. the CaMV 35S-promoter of the cauliflower-mosaic-virus (Franck et al., Cell 21, 285-294 (1980)). Expression of the nucleic acid sequence of this invention may also be achieved by a chemical inducible promoter. Examples for chemical inducible promoters are the PRPI-~~Promoter~~promoter (Ward et al., Plant Molecular Biology 22, 361-366 (1993)), a salicylic acid inducible promoter (WO 95/19443), a benzenesulfonamide inducible promoter (EP-A 388186), a tetracyclin ~~inducable~~inducible promoter (Gatz et al., Plant Journal 2, 397-404 (1992)), a abscisic acid inducible promoter (EP-A 335528) as well as a ethanol or ~~cyclohexanon~~cyclohexanone inducible promoter (WO 93/21334). Depending on the desired location of expression also promoters may be used, which are active in certain plant tissues or plant parts. Examples for corresponding promoters are the phaseolin promoter (US 5504200), the ~~isoflavon~~isoflavone reductase promoter (US 5750399), a seed specific promoter from tobacco (US 5824863) or the ST-LSI promoter from potato (Stockhaus et al., EMBO Journal 8, 2445-2452 (1989)).

At page 2, lines 26-33; page 3, lines 1-23, please replace the paragraphs with the following:

Figure 1 shows a schematic representation of the analysis of the nucleic acid sequence of the TT1-promoter (SEQ ID NO:1) in comparison with TRANSFAC MATRIX TABLE, Rel.3.3 (E. Wingender et al., 1998). Binding sites for transcription factors are indicated

by capital letters (SBF-1 like sites: see Lawton et al, Silencer region of a chalcone synthase promoter contains multiple binding sites for a factor, SBF-1, closely related to GT-1, Plant Molecular Biology 16, 235-249 (1991)), in italics (AGAMOUS like sites: Huang et al., isolation and characterization of the binding sequences for the product of the Arabidopsis floral homeotic gene AGAMOUS, Nucleic Acids Research 21, 4769-4776 (1993)), underlined letters (P like sites: Grotewold et al., The myb-homologous P gene controls phlobabene pigmentation in maize floral organs by directly activating a flavonoid biosynthetic gene subset, Cell 76, 543-553 (1994)), capital and italic letters (MYB Ph3 like sites: Solano et al., Dual DNA binding specifity of a petal epidermis-specific MYB transcription factor (MYB.PH3) from Petunia hybrida, EMBO Journal 14, 1773-1784 (1995)) as well as capital and underlined letters (Athab-1 und 2 like sites: Sessa et al., The athb-1 and -2 HD-Zip domains homodimerize forming complexes of different DNA binding specificities, EMBO Journal 12, 3507-3517 (1993)). The start-ATG is indicated by bold and underlined letters. Numbering starts with the 5' SpeI restriction site in the used plasmid vector pSK-TT1.

Figure 2 shows the nucleic acid sequence of the genomic DNA sequence of TT1 (SEQ ID NO:4), commencing with the start-ATG. Capitals represent exons, introns are in italics. Numbering resumes the one of figure 1.

Figure 3 shows the cDNA sequence, encoding the TT1 gene and the predicted amino acid sequence of TT1 (SEQ ID NO:2 and SEQ ID NO:3).

Figure 4 shows schematically an alignment of the amino acid sequence of TT1 with sequences of the NCBI GenBank. acc. No AL049660, AB025629 and AC006085.9 are hypothetical amino acid sequences derived from nucleic acid sequences of *Arabidopsis thaliana* (At), AJ234704 is a hypothetical amino acid sequence derived from a nucleic acid sequence of *Hordeum vulgare* (Hv). In the consensus sequence a ! denotes amino acids of the type I or V, a $ amino acids of the type L or M, a % amino acids of the type F or Y and a # amino acids of the type N, D, Q, E, B or Z (SEQ ID NOS:3, 5, 6, 7 and 8).